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Research Article

A new revision of the lichen genus *Pleopsidium* (Acarosporales, Acarosporaceae) in China reveals two new species

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Abstract

Based on a combination of morphological, chemical, and phylogenetic analyses, we present a new revision of the lichen genus *Pleopsidium* in China. *Pleopsidium tumidulum* **sp. nov.** and *P. corrugatulum* **sp. nov.** are proposed as new species to science, both included in a distinctive clade (clade 1) together with *P. gobiense*. These three species are characterized by the absence of fatty acids, acaranoic and acarenoic acids, and share similar ecological traits. In contrast, species containing fatty acids, including *Pleopsidium flavum*, *P. chlorophanum*, and *P. discurrens*, constitute a separate clade (clade 2). Fresh specimens of *Pleopsidium discurrens* were collected from the type locality, Yulong Snow Mountain, and molecular data were generated to confirm the phylogenetic position of the species. Our study additionally reveals substantial morphological variation in this species. New collections and sequences of *Pleopsidium gobiense* from Hami City, the type locality, are provided, from which a neotype is designated, confirming its phylogenetic position. Differences in morphology, anatomy, chemistry, and ecology among *Pleopsidium* species from China are discussed. A key and several phylograms are provided.

Key words: Lichenized fungi, neotype, phylogeny, saxicolous yellow species, taxonomy

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Introduction

Pleopsidium Körb. was first described in 1855 (Körber 1855). In the early 20th century, Magnusson (1924), Paulson (1925), and Räsänen (1943) considered *Pleopsidium* as a section of *Acarospora* A. Massal. After a detailed comparison with other similar species in *Acarospora* and *Lecanora* Ach., Hafellner (1993) reinstated *Pleopsidium* to the generic rank on the basis of ascus structure, pycnidia, upper cortex anatomy, secondary chemistry, habitat, ecology, and biogeography.

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Later phylogenetic research by Westberg et al. (2015) concluded that *Pleopsidium* species form a distinct group well separated from other genera in Acarosporaceae.

Pleopsidium includes four species characterized by a yellow upper surface, marginal lobes, *Pleopsidium*-type asci, and numerous spores. It also contains rhizocarpic acid and sometimes acaranoic, acarenoic, and lichesterinic fatty acids. Species of *Pleopsidium* are distributed in Antarctica, Asia, Europe, and North and South America (Wei 1991; Brodo et al. 2001; Nash III et al. 2007; Knudsen et al. 2008). *Pleopsidium chlorophanum* (Wahlenb.) Arnold and *P. flavum* (Bellardi) Körb. were described from Europe (Hafellner 1993). Although they have been reported from China, these records need to be confirmed by molecular data (Paulson 1925, 1928; Moberg 1996; Niu et al. 2015, 2017; Aerguli et al. 2018). *Pleopsidium gobiense* (H. Magn.) Hafellner is widely distributed in the deserts of Central Asia and has been reported from similar habitats in China (Magnusson 1940, 1944; Niu et al. 2015, 2017; Aerguli et al. 2018). *Pleopsidium discurrens* (Zahlbr.) Obermayer was described from Yunnan and Sichuan and was later also reported from Tibet, China (Zahlbruckner 1930; Obermayer 1996).

The nomenclature was disputed for "*Pleopsidium oxytonum* (Ach.) Rabenh." and "*Pleopsidium flavum* (Bell.) Körber," but more recently, *Pleopsidium oxytonum* has been treated as a later synonym of *P. flavum* (Knudsen and Arcadia 2018). *Pleopsidium stenosporum* (Stizenb. ex Hasse) K. Knudsen, reported from North America, had also been treated as a synonym of *P. flavum* due to its similar morphology and chemistry (Knudsen 2011; Knudsen and Kocourková 2013). During our studies of *Pleopsidium* specimens in China, two new species were discovered based on integrated phenotypic and molecular analyses. These species are described and characterized below. In this study, we assign a total of six species to *Pleopsidium*.

Materials and methods

Morphological and chemical analyses

Specimens of *Pleopsidium* were mainly collected during expeditions across the Qinghai–Tibetan Plateau from 2018 to 2023. In this study, 130 specimens were examined and deposited in the Kunming Institute of Botany (China) herbarium (KUN) and the Arid Land Lichen Research Center of Western China, Xinjiang University (Urumqi, China) herbarium (XJU). Morphological and anatomical characters of thalli and apothecia were examined under a dissecting microscope (Nikon SMZ 745T) and an optical microscope (Nikon Eclipse Ci-S). Descriptions of the range of anatomical characters were based on the smallest and largest single values measured at 400× or 1000× magnification for all specimens. Photos were taken with a digital camera (Nikon Z5) and a stereomicroscope (Zeiss Axio Scope A1). The thallus and medulla were tested with K (a 10% aqueous solution of potassium hydroxide), C (a saturated aqueous solution of sodium hypochlorite), and P (a saturated solution of *p*-phenylenediamine in 95% ethyl alcohol) for identification. Secondary metabolites were identified using standardized thin-layer chromatography (TLC) with solvent system C (toluene:acetic acid = 85:15; Orange et al. 2001).

DNA extraction, amplification, and sequencing

DNA was extracted from small fragments of fresh thallus tips or apothecia using a DNAsecure Plant Kit (TIANGEN) according to the manufacturer's instructions. The following regions were amplified: the internal transcribed spacer region (ITS1–5.8S–ITS2), the nuclear large subunit rDNA gene (nuLSU), and the mitochondrial small subunit rDNA gene (mtSSU). The primers used were ITS1F (Gardes and Bruns 1993) and ITS4 (White et al. 1990), LR0R (Rehner and Samuels 1994) and LR5 (Vilgalys and Hester 1990), and mtSSU1 and mtSSU3R (Zoller et al. 1999), respectively. PCR amplifications were carried out in a 25 µL reaction volume containing 2 µL of genomic DNA, 1 µL of 10 mM solution for each primer, 12.5 µL of 2× T3 Taq PCR Mix (TSINGKE), and 8.5 µL of ddH_2O. The PCR profile was initial denaturation at 94 °C for 5 min, followed by 30 cycles of 94 °C for 1 min, 54–56 °C for 1 min, and 72 °C for 1 min 30 s, with a final extension at 72 °C for 7 min in an automatic thermocycler. The PCR products were sequenced using the same amplification primers via Sanger technology by Sangon Biotech (Shanghai, China).

Phylogenetic analyses

All raw sequences were assembled and edited using MAFFT v.7 in Geneious v8.0.2 with the default settings (Katoh et al. 2005; Katoh and Standley 2013). A 3-locus (nuITS–nuLSU–mtSSU) concatenated matrix was generated using *Pleopsidium* species sequences and sequences from related genera in Acarosporaceae (Table 1). Congruence between different gene regions was analyzed before combining sequences. The nuITS dataset consists of 57 newly generated sequences and 54 sequences from GenBank (Tables 1, 2). The nuLSU dataset consists of 21 sequences (Table 1). The final matrices are provided in the Suppl. materials 1, 2, 3: nuITS, nuLSU, and the 3-locus concatenated matrix. Bayesian inference (BI) and maximum likelihood (ML) were used to reconstruct the phylogenetic trees. Based on the lowest Bayesian information criterion (BIC), the best-fit partition substitution models were selected using PartitionFinder 2 (Lanfear et al. 2016) and RAxML (Stamatakis 2014) in PhyloSuite (Zhang et al. 2020) for the following ML and BI analyses: the nuITS dataset (TIM2e+G4) and the 3-locus concatenated matrix (GTR+I+G for each subset).

ML analyses were performed using IQ-TREE v.1.6.12 (Nguyen et al. 2015). Bootstrap frequencies were estimated from the consensus tree built with trees obtained from 2000 non-parametric bootstrapping pseudo-replicates. Bootstrap support values (MLBS) were obtained from the 70% majority rule tree of all saved trees. BI analyses were performed using MrBayes v3.2.6 (Ronquist et al. 2012). Markov chain Monte Carlo algorithms with four incrementally heated chains were run for 2 million generations to implement the BI analyses. Trees were sampled every 100 generations, and the first 25% of trees were discarded as burn-in. The stop rule was the average standard deviation of split frequencies < 0.01. Bayesian posterior probabilities (BPP) were obtained from the 95% majority rule consensus tree of all saved trees. The final trees were visualized using FigTree v1.4.0 (Rambaut 2012).

Table 1. Sequences and specimens in the phylogenetic tree. Newly obtained sequences are in bold. "Null" indicates that no sequences were available.

Taxon name	Voucher	Locality	GenBank accession number		
			nuITS	nuLSU	mtSSU
Acarospora schleicheri 1	Obermayer 2919	China: Sichuan	LN810800	LN810800	LN810925
A. schleicheri 2	Sweat & Yansky KGS1196	USA: Arizona	LN810801	LN810801	LN810926
A. umbilicata	Tibell 23532 (UPS)	Sweden	LN810808	LN810808	LN810933
Glypholecia qinghaiensis 1	22-71630	China	OP749916	NULL	OP749899
G. qinghaiensis 2	20-68255	China	MZ330789	NULL	OP749910
G. scabra 1	Westberg 08-232 (S)	Norway	LN810811	LN810811	LN810936
G. scabra 2	AFTOL-ID 1008	/	HQ650722	NULL	KJ766399
G. scabra 3	19-66159	China	MZ330790	NULL	OP749909
Myriospora myochroa	Halda & Palice 1382	Czech	EU870677	NULL	EU870729
M. rhagadiza	Westberg 06-034	Sweden	EU870646	LN810876	EU870698
M. scabrida	Westberg 2824	Norway	EU870643	LN810877	EU870695
M. smaragdula	Wedin 6620 (UPS)	Sweden	EU870688	LN810879	EU870740
M. tangerina	Crewe 104 (UPS)	Greenland	EU870683	NULL	EU870735
Pleopsidium chlorophanum 1	Nordin 6209 (UPS)	Sweden	LN810813	LN810813	LN810938
P. chlorophanum 2	Knudsen 16955	Austria	ON303961	ON303965	ON303852
P. chlorophanum 3	Nordin 4439 (UPS)	Sweden	EU870691	LN810881	EU870743
P. chlorophanum 4	Wedin 6589 (UPS)	Sweden	AY853384	AY853384	AY853335
P. chlorophanum 5	AFTOL-ID 1004 (DUKE)	/	NULL	DQ842017	DQ991756
P. chlorophanum	ZYY-137	Austria	**PQ877185**	**PQ871181**	**PQ871158**
P. corrugatulum	20151086-c	China: Ningxia	**MN129010**	**MN129034**	**MN129047**
P. corrugatulum	20130708-1	China: Xinjiang	**MN129009**	**MN129033**	**MN129046**
P. corrugatulum	ZSB23-906	China: Qinghai	**PQ877160**	**PQ871169**	**PQ871146**
P. corrugatulum	22-72992	China: Xinjiang	**PQ877161**	**PQ871179**	**PQ871156**
P. corrugatulum	22-72341	China: Xinjiang	**PQ877162**	**PQ871180**	**PQ871157**
P. corrugatulum	ZYJ1	China: Ningxia	**PQ877163**	**PQ871182**	**PQ871159**
P. discurrens	15-49590	China: Yunnan	**MN129017**	**MN129040**	**MN129054**
P. discurrens	17-56207	China: Yunnan	**PQ877170**	**PQ871163**	**PQ871138**
P. discurrens	17-55117a	China: Yunnan	**PQ877171**	**PQ871164**	**PQ871139**
P. discurrens	17-55054	China: Yunnan	**PQ877172**	**PQ871165**	**PQ871140**
P. discurrens	23-74275	China: Yunnan	**PQ877175**	NULL	**PQ871143**
P. discurrens	23-74395	China: Yunnan	**PQ877176**	NULL	**PQ871144**
P. flavum 1	Malicek	Czech	OK142757	OP497841	OK032142
P. flavum 2	Obermayer 7790	Austria	AY853385	AY853385	AY853336
P. flavum 3	Burgaz 2004 (H)	/	NULL	KJ766628	KJ766462
P. flavum 4	Spribille 40380 (GZU)	USA: Montana	NULL	NULL	MN508323
P. gobiense 1	AFTOL-ID 1003	/	HQ650723	DQ883698	DQ991755
P. gobiense 2	Moberg & Nordin (UPS)	Kazakhstan	DQ374144	NULL	DQ374123
P. gobiense	Pg161008-1	China: Xinjiang	**MN129006**	**MN129030**	**MN129043**
P. gobiense	Pc161016-1	China: Xinjiang	**MN129007**	**MN129031**	**MN129044**
P. gobiense	2014011A-1	China: Xinjiang	**MN129008**	**MN129032**	**MN129045**
P. gobiense	LD22-513	China: Xinjiang	**PQ877166**	**PQ871177**	**PQ871154**
P. gobiense	XY22-947	China: Xinjiang	**PQ877167**	**PQ871178**	**PQ871155**
P. gobiense	XJ-ZSB23-119	China: Xinjiang	**PQ877165**	**PQ871173**	**PQ871150**
P. tumidulum	18-58228	China: Qinghai	**PQ877140**	**PQ871166**	**PQ871141**
P. tumidulum	20157527-1	China: Neimenggu	**PQ877141**	**PQ871167**	**PQ871142**
P. tumidulum	ZSB24-1392	China: Qinghai	**PQ877152**	**PQ871172**	**PQ871149**
P. tumidulum	ZSB23-545	China: Qinghai	**PQ877150**	**PQ871170**	**PQ871147**
P. tumidulum	ZSB24-1363	China: Qinghai	**PQ877147**	**PQ871168**	**PQ871145**
P. tumidulum	ZSB24-1400	China: Qinghai	**PQ877151**	**PQ871171**	**PQ871148**
P. tumidulum	XY22-896	China: Xinjiang	**PQ877155**	**PQ871175**	**PQ871152**
P. tumidulum	ZYY22-558	China: Xinjiang	**PQ877154**	**PQ871174**	**PQ871151**
P. tumidulum	XY22-773	China: Xinjiang	**PQ877156**	**PQ871176**	**PQ871153**
Polysporina simplex	Westberg SAR273 (S)	Austria	LN810826	LN810826	LN810951

Taxon name	Voucher	Locality	GenBank accession number		
			nuITS	nuLSU	mtSSU
Po. subfuscescens	Westberg 08-154 (S)	Norway	LN810832	LN810832	LN810958
Pycnora sorophora	Hermansson 7903a (UPS)	Sweden	FJ959357	AY853387	AY853338
Sarcogyne distinguenda	Westberg 08-305 (S)	Sweden	LN810854	LN810854	LN810979
S. hypophaea	Westberg SAR198 (S)	Sweden	LN810856	LN810856	LN810981
S. regularis	Westberg 08-034 (S)	Sweden	LN810861	LN810861	LN810986
Timdalia intricata 1	Westberg P114 (S)	Sweden	LN810867	LN810867	LN810992
T. intricata 2	Westberg SAR92 (LD)	Sweden	LN810866	KP794969	LN810991

Results

The 3-locus (nuITS, nuLSU, and mtSSU) concatenated matrix comprised 167 terminals (513 bp for 57 nuITS, 838 bp for 50 nuLSU, and 751 bp for 60 mtSSU), which included 82 newly generated *Pleopsidium* sequences (Table 1). Six representative monophyletic genera—*Acarospora*, *Glypholecia* Nyl., *Myriospora* Nägeli ex Uloth, *Polysporina* Vězda, *Sarcogyne* Flot., and *Timdalia* Hafellner—were selected from Acarosporaceae, and *Pycnora sorophora* (Vain.) Hafellner was selected as the outgroup. The phylogenetic analyses showed that the genus *Pleopsidium* is located within Acarosporaceae, but this position was not highly supported (Fig. 1). Relationships between *Pleopsidium* and other genera within Acarosporaceae still require further research. Two distinct clades were formed within *Pleopsidium* (Fig. 1).

In clade 1, *Pleopsidium gobiense*, *P. corrugatulum*, and *P. tumidulum* formed a monophyletic clade with strong support (100% BS and 1.00 PP). Specimens here described as *Pleopsidium corrugatulum* formed a well-supported sister clade to *P. gobiense* (100% BS and 1.00 PP). These two species differ in their anatomical characteristics. Therefore, we recognize *Pleopsidium corrugatulum* as a new species. The collections designated as *Pleopsidium tumidulum* were clustered as a single lineage with high support (100% BS and 1.00 PP) and have also been introduced as a new species for China. These three species are similar in chemistry and ecology: they are characterized by the absence of fatty acids and share a Central Asian distribution. A detailed comparison of their differences is provided in the Discussion section.

In clade 2, *Pleopsidium flavum*, *P. chlorophanum*, and *P. discurrens* formed an independent clade with high support (96% BS and 1.00 PP). *Pleopsidium flavum* (the type species of *Pleopsidium*) formed a single clade with strong support (100% ML and 1.00 PP). *Pleopsidium chlorophanum* and *P. discurrens* also formed a distinct monophyletic clade with high support (100% ML and 1.00 PP). Fatty acids were detected within the thalli of all three species (Hafellner 1993; Obermayer 1996). Sequences of *Pleopsidium flavum* and *P. chlorophanum* were downloaded from GenBank. Specimen No. ZYY-137 is preserved at the KUN herbarium but was originally collected from Austria. The distribution of these two species has not previously been confirmed in China. A detailed discussion is given below.

Discussion

Phylogeny of *Pleopsidium*

The phylogenetic trees illustrate that *Pleopsidium* species form two highly supported monophyletic lineages (Fig. 1), both in the single-region phylogeny (nuITS; Fig. 2) and the combined-region phylogeny (nuITS–nuLSU–mtSSU; Fig. 1). Species within

Table 2. nuITS sequences and specimens. Newly obtained sequences are in bold.

Taxon name	Voucher	Locality	nuITS GenBank accession number
Pleopsidium chlorophanum 6	Keller 15669	Austria	DQ525482
P. chlorophanum 7	Haugan SK00-117	Norway	DQ525484
P. chlorophanum 8	Nimis & Tretiach 25181 (TSB)	Russia	DQ525488
P. chlorophanum 9	Sipman Tan & Reiniko 23368	Finland	DQ525489
P. chlorophanum 10	Arup L98077	Austria	EF535222
P. chlorophanum 11	O-L-184414	Norway	MK812213
P. chlorophanum 12	O-L-208244	Norway	MK812354
P. chlorophanum 13	Engelskjøn (BGL-500713)	Dronning Maud Land	DQ525485
P. corrugatulum	20151024-a	China: Ningxia	**PQ877158**
P. corrugatulum	Po001003	China: Xinjiang	**MN129011**
'P. flavum'	20141215-1	China: Neimenggu	**PQ877159**
'P. flavum'	20141062-a	China	MF188905
'P. gobiense' 1	Huneck MVR88-47 (B600095250)	Mongolia	DQ525492
'P. gobiense' 2	Huneck MVR88-304 (B600095255)	Mongolia	DQ525493
'P. gobiense' 3	Reeb VR 14-VII-04/6 (DUKE)	Mongolia	DQ525494
P. discurrens	Obermayer 5127 (GZU)	China: Xizang	DQ525510
P. discurrens	16-53097	China: Xizang	**PQ877169**
P. discurrens	17-55117b	China: Yunnan	**MN129016**
P. discurrens	12-34822	China: Yunnan	**PQ877173**
P. discurrens	18-60699	China: Yunnan	**PQ877174**
P. discurrens	19-65574	China: Xizang	**PQ877177**
P. discurrens	19-63921	China: Xizang	**PQ877179**
P. discurrens	19-64991	China: Xizang	**PQ877180**
P. discurrens	19-64053	China: Xizang	**PQ877181**
P. discurrens	19-63666	China: Xizang	**PQ877182**
P. discurrens	19-63913	China: Xizang	**PQ877183**
P. discurrens	19-65758	China: Xizang	**PQ877184**
P. discurrens	19-65351	China: Xizang	**PQ877178**
P. flavum 5	M0062614	USA	DQ525500
P. flavum 6	Reeb VR 22-VIII-99/4b (DUKE)	Poland	DQ525507
P. flavum 7	Reeb VR 2-IX-00/15 (DUKE)	Spain	DQ525521
P. flavum 8	Grisons, Scheidegger	Switzerland	DQ525514
P. flavum 9	Reeb VR 31-VIII-00/1 (DUKE)	Spain	DQ525515
P. flavum 10	B600125577	Bulgaria	DQ525516
P. flavum 11	John & Zeybek 6.167 (B600125572)	Turkey	DQ525517
P. flavum 12	Leavitt 18-300 BRY-C	USA: Utah	MZ243480
P. flavum 13	Leavitt 18-355 BRY-C	USA: Utah	MZ243479
P. gobiense 3	Vost, Moberg & Nordin (M0062472)	Kazakhstan	DQ525496
P. gobiense 4	Golubkova & Zogt 431 (DUKE)	Mongolia	DQ525497
P. gobiense	20122500	China: Xinjiang	**PQ877164**
P. gobiense	22-72982	China: Xinjiang	**PQ877168**
P. tumidulum	18-59258	China: Qinghai	**PQ877139**
P. tumidulum	20-67122	China: Qinghai	**PQ882529**
P. tumidulum	22-71718	China: Xinjiang	**PQ882528**
P. tumidulum	20-67124	China: Qinghai	**PQ877143**
P. tumidulum	22-72854	China: Xinjiang	**PQ877145**
P. tumidulum	ZSB23-1219	China: Qinghai	**PQ877153**
P. tumidulum	XJ-ZSB23-041	China: Xinjiang	**PQ877148**
P. tumidulum	ZSB23-538	China: Qinghai	**PQ877149**
P. tumidulum	LD22-468	China: Xinjiang	**PQ877157**
P. tumidulum	22-72874	China: Xinjiang	**PQ877146**
P. tumidulum	22-72216	China: Xinjiang	**PQ877144**
'P. flavum'	20121958-1	China: Neimenggu	**PQ877142**
'P. chlorophanum'	20157538	China: Neimenggu	MF188904
'P. chlorophanum'	Pc920702	China: Xinjiang	MF188906

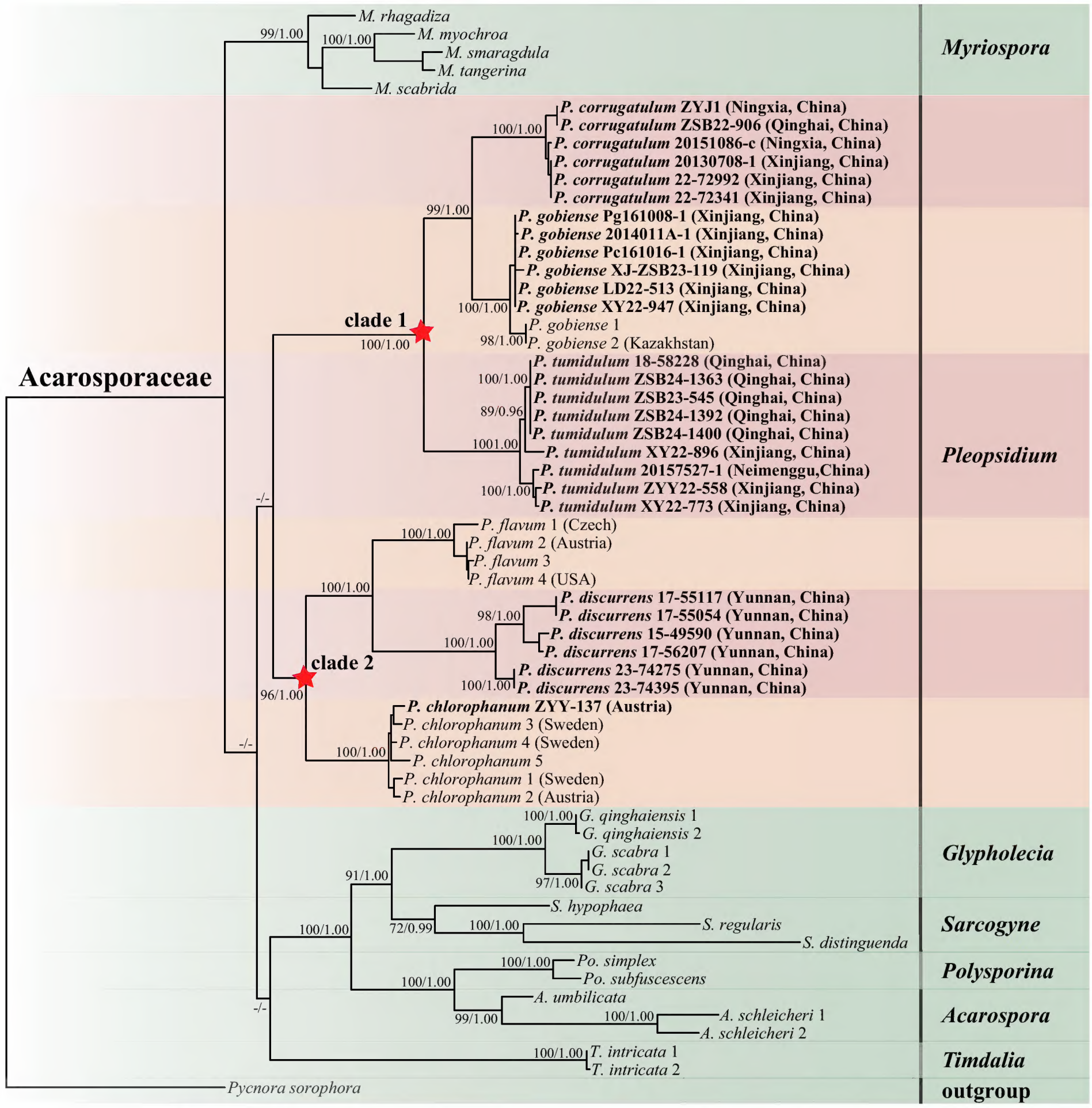

Figure 1. Maximum likelihood (ML) phylogenetic tree of *Pleopsidium* and selected Acarosporaceae species based on phylogenetic analysis of the nuITS–nuLSU–mtSSU concatenated sequence matrix. Newly obtained sequences are in bold. Maximum likelihood bootstrap support values (MLBS) and Bayesian posterior probabilities (PP) are given near the nodes.

clade 1 do not contain fatty acids, whereas species within clade 2 contain fatty acids such as acaranoic or acarenoic acids. These two clades could be treated as different genera based on chemical and molecular evidence. The genus concept of *Pleopsidium* would then require revision, with species that lack fatty acids being excluded from *Pleopsidium*. However, such a taxonomic proposal would be unsupported by morphological evidence. The relationships between these two clades and other Acarosporaceae genera require further clarification. We therefore maintain the current circumscription of the genus. The phylogeny of Acarosporaceae requires further research, including the collection of additional samples from other regions of the world and molecular data for other genera within Acarosporaceae.

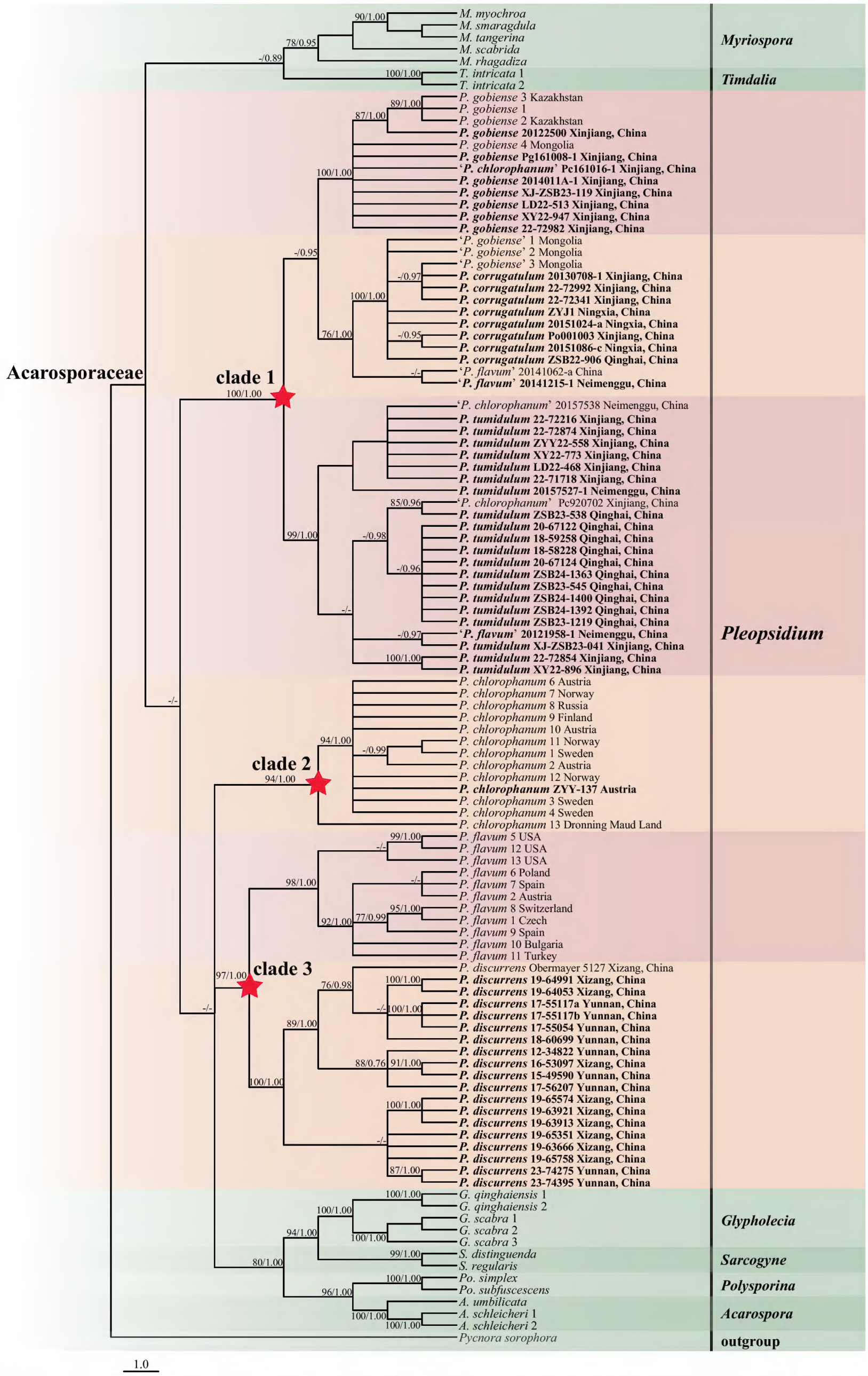
Acarosporaceae
clade 1
clade 2
clade 3
M. myochroa
M. smaragdula
M. tangerina
M. scabrida
M. rhagadiza
T. intricata 1
T. intricata 2
P. gobiense 3 Kazakhstan
P. gobiense 1
P. gobiense 2 Kazakhstan
P. gobiense 20122500 Xinjiang, China
P. gobiense 4 Mongolia
P. gobiense Pg161008-1 Xinjiang, China
'P. chlorophanum' Pc161016-1 Xinjiang, China
P. gobiense 2014011A-1 Xinjiang, China
P. gobiense XJ-ZSB23-119 Xinjiang, China
P. gobiense LD22-513 Xinjiang, China
P. gobiense XY22-947 Xinjiang, China
P. gobiense 22-72982 Xinjiang, China
'P. gobiense' 1 Mongolia
'P. gobiense' 2 Mongolia
'P. gobiense' 3 Mongolia
P. corrugatulum 20130708-1 Xinjiang, China
P. corrugatulum 22-72992 Xinjiang, China
P. corrugatulum 22-72341 Xinjiang, China
P. corrugatulum ZYJ1 Ningxia, China
P. corrugatulum 20151024-a Ningxia, China
P. corrugatulum Po001003 Xinjiang, China
P. corrugatulum 20151086-c Ningxia, China
P. corrugatulum ZSB22-906 Qinghai, China
'P. flavum' 20141062-a China
'P. flavum' 20141215-1 Neimenggu, China
'P. chlorophanum' 20157538 Neimenggu, China
P. tumidulum 22-72216 Xinjiang, China
P. tumidulum 22-72874 Xinjiang, China
P. tumidulum ZYY22-558 Xinjiang, China
P. tumidulum XY22-773 Xinjiang, China
P. tumidulum LD22-468 Xinjiang, China
P. tumidulum 22-71718 Xinjiang, China
P. tumidulum 20157527-1 Neimenggu, China
'P. chlorophanum' Pc920702 Xinjiang, China
P. tumidulum ZSB23-538 Qinghai, China
P. tumidulum 20-67122 Qinghai, China
P. tumidulum 18-59258 Qinghai, China
P. tumidulum 18-58228 Qinghai, China
P. tumidulum 20-67124 Qinghai, China
P. tumidulum ZSB24-1363 Qinghai, China
P. tumidulum ZSB23-545 Qinghai, China
P. tumidulum ZSB24-1400 Qinghai, China
P. tumidulum ZSB24-1392 Qinghai, China
P. tumidulum ZSB23-1219 Qinghai, China
'P. flavum' 20121958-1 Neimenggu, China
P. tumidulum XJ-ZSB23-041 Xinjiang, China
P. tumidulum 22-72854 Xinjiang, China
P. tumidulum XY22-896 Xinjiang, China
P. chlorophanum 6 Austria
P. chlorophanum 7 Norway
P. chlorophanum 8 Russia
P. chlorophanum 9 Finland
P. chlorophanum 10 Austria
P. chlorophanum 11 Norway
P. chlorophanum 1 Sweden
P. chlorophanum 2 Austria
P. chlorophanum 12 Norway
P. chlorophanum ZYY-137 Austria
P. chlorophanum 3 Sweden
P. chlorophanum 4 Sweden
P. chlorophanum 13 Dronning Maud Land
P. flavum 5 USA
P. flavum 12 USA
P. flavum 13 USA
P. flavum 6 Poland
P. flavum 7 Spain
P. flavum 2 Austria
P. flavum 8 Switzerland
P. flavum 1 Czech
P. flavum 9 Spain
P. flavum 10 Bulgaria
P. flavum 11 Turkey
P. discurrens Obermayer 5127 Xizang, China
P. discurrens 19-64991 Xizang, China
P. discurrens 19-64053 Xizang, China
P. discurrens 17-55117a Yunnan, China
P. discurrens 17-55117b Yunnan, China
P. discurrens 17-55054 Yunnan, China
P. discurrens 18-60699 Yunnan, China
P. discurrens 12-34822 Yunnan, China
P. discurrens 16-53097 Xizang, China
P. discurrens 15-49590 Yunnan, China
P. discurrens 17-56207 Yunnan, China
P. discurrens 19-65574 Xizang, China
P. discurrens 19-63921 Xizang, China
P. discurrens 19-63913 Xizang, China
P. discurrens 19-65351 Xizang, China
P. discurrens 19-63666 Xizang, China
P. discurrens 19-65758 Xizang, China
P. discurrens 23-74275 Yunnan, China
P. discurrens 23-74395 Yunnan, China
G. qinghaiensis 1
G. qinghaiensis 2
G. scabra 1
G. scabra 2
G. scabra 3
S. distinguenda
S. regularis
Po. simplex
Po. subfuscescens
A. umbilicata
A. schleicheri 1
A. schleicheri 2
Pycnora sorophora
Myriospora
Timdalia
Pleopsidium
Glypholecia
Sarcogyne
Polysporina
Acarospora
outgroup
1.0

Figure 2. Maximum likelihood (ML) phylogenetic tree of the genus *Pleopsidium* and selected species of Acarosporaceae based on phylogenetic analysis of the nuITS sequence matrix. Newly obtained sequences are in bold. Maximum likelihood bootstrap support values (MLBS) and Bayesian posterior probabilities (PP) are given near the nodes.

Species delimitation of *Pleopsidium*

Species in *Pleopsidium* have similar morphological and chemical characters. Molecular data could help to resolve and identify such cryptic taxa.

The three species in clade 1 (Fig. 1) share the absence of fatty acids but show morphological differences. *Pleopsidium tumidulum* has convex, plump, swollen, and smooth long lobes (2.5–4.5 mm), a thick thallus (up to 1.5–3.0 mm), and can be reliably recognized by its wide apothecia (1.5–2.5 mm). Both *Pleopsidium corrugatulum* and *P. gobiense* have thinner thalli (<1.5 mm), short lobes (<3 mm long), and smaller apothecia (up to 1.25 mm). There are only minor morphological differences between *Pleopsidium corrugatulum* and *P. gobiense*, potentially due to their similar habitats. *Pleopsidium gobiense* has numerous apothecia and few pycnidia, and the apothecia are plane, nearly flat to the thallus. In *Pleopsidium corrugatulum*, only a few specimens have apothecia, whereas most have many pycnidia.

Molecular data provided significant support for distinguishing among these three species. The nuLSU gene was highly variable (Fig. 3). For nuLSU barcode sequences designed to identify these three species, BLASTn top-scoring hits matched the species identity inferred from our phylogenetic inferences (Suppl. material 4), demonstrating the reliability of the short barcodes.

The specimens of *Pleopsidium discurrens* in clade 2 (Fig. 1) showed variable morphology, but few molecular differences were detected. Materials from the type locality, the Hengduan Mountains region, showed typical ribbon-like, elongate, branched, and spreading lobes, which is the distinctive character of this species. However, specimens from alpine desert regions had different morphology, with much shorter and more aggregated lobes. Molecular data indicate that they belong to the same species (Fig. 2). The morphological differences may be due to adaptation to a drier environment. This warrants further investigation using specimens collected across different climatic zones.

A

nuLSU matrix 839–905 bp (Suppl. material 2)

corresponding to positions 839–871 bp of the reference sequence GenBank: PQ871169

P. tumidulum	TGTTGGCAGCACGTKAAAGATT–GTCCAGTTTGTAGAGTATACATTCGAAAAGTCTTTCTCCGCAGC
P. gobiense	CATTGGCGGCACAGCAATGATTTGTCC——————————————————————————CGTAGC
P. corrugatulum	CATTGGCGGCACATGAATGATTTGTCC——————————————————————————CGCGGC

B

nuLSU matrix 1035–1072 bp (Suppl. material 2)

corresponding to positions 999–1036 bp of the reference sequence GenBank: PQ871169

P. tumidulum	TTGTTTTCTCCAG——————————TGAAGGAAAT
P. gobiense	CCGTTCCCTCAACACCCCAACTGTCAGTTGAAGGGAAT
P. corrugatulum	CTGTTCTCTCAACACCTCAACTGGCAGTTGGAGGGAAC

Figure 3. Alignment of nucleotide sequences within a portion of nuLSU, allowing identification of the three recognized species that lack fatty acids. Deviations are in red font, and short lines represent nucleotides that are not present. The IUPAC ambiguity code is used. **A.** Position 839–905 bp; **B.** Position 1035–1072 bp.

Misidentifications

Pleopsidium chlorophanum was reported by Paulson (1925, 1928) and referenced also by Zahlbruckner (1930) and Obermayer (1996) from Mount Everest and northwestern Yunnan in China. We examined specimens from Yunnan, Xizang, Xinjiang, Qinghai, Ningxia, and Neimenggu provinces in China but did not find further examples of the species. Niu et al. (2017) also reported *Pleopsidium chlorophanum* but detected calycin in those specimens—a compound known to be present in morphologically similar species of *Lecanora* (Yakovchenko et al. 2019). We re-examined specimens [02-21440 (KUN), 04-25611 (KUN), and 14-45562 (KUN)] that had eight-spored asci and confirmed that they clearly did not belong to *Pleopsidium* but were misidentifications of *Lecanora*. Aerguli et al. (2018) identified some specimens from Xinjiang and Neimenggu as *Pleopsidium chlorophanum*. Sequences of the two specimens (20157538, Pc920702) cited by Aerguli et al. (2018) were clustered with *Pleopsidium tumidulum*. These two specimens both lacked fatty acids. The specimen Pc161016-1 also lacked fatty acids, and its sequence clustered with *Pleopsidium gobiense* (Fig. 2).

Some old specimens from Xizang and Yunnan had been identified as *Pleopsidium flavum* by Niu et al. (2017). However, we have surveyed those regions on multiple occasions and only found samples of *Pleopsidium discurrens*. Some specimens with atypical morphology of *Pleopsidium discurrens* could easily be misidentified as *P. flavum*. After examining additional specimens, we re-identified five specimens cited as *Pleopsidium flavum* by Niu et al. (2017) as *P. discurrens*. Four specimens classified as *Pleopsidium flavum* by Aerguli et al. (2018) were also revised based on chemical and molecular analyses: *P. corrugatulum* (20151068, 20141215-1, 20141062-a) and *P. tumidulum* (20121958-1) (Fig. 2).

Despite extensive field surveys and phylogenetic analysis, we have not found *Pleopsidium chlorophanum* or *P. flavum* in China. Further comprehensive surveys are required to confirm whether these species are present in the country.

Taxonomy

***Pleopsidium corrugatulum* C. C. Miao, Xin Y. Wang & Li S. Wang, sp. nov.**
MycoBank No: 859408
Figs 4, 5

Type. China. • Qinghai Prov.: Xining Ci., 36°33'17"N, 101°54'01"E, alt. 2190 m, 07 Jul. 2023, S.B. Zhang et al. ZSB23-906 (holotype: KUN; isotype: SDNU).

Diagnosis. The new species differs from *Pleopsidium tumidulum* by its wrinkled areoles surface, thinner thalli, shorter lobes, numerous pycnidia, and molecular data.

Description. Thallus crustose, tightly attached to the substrate, areolate at center, radiate-plicate at margin; areoles rimose, wrinkled, mostly infertile, 1–2.3 × 0.8–1.5 mm; marginal lobes sometimes cracked, 1–3 mm long, 1–2 mm wide, 0.7–1.5 mm thick, tightly attached to the substrate; upper surface yellow or dark yellowish green; upper cortex yellow, 25–50 µm thick; algal layer 100–175 µm thick; medulla white, 100–275 µm thick. Apothecia rare to moderately frequent, one mature apothecium or several young ones in each areola, cryptolecanorine to lecanorine, roundish, 0.9–1.25 mm wide; disc pale

Figure 4. *Pleopsidium corrugatulum* in its habitat.

yellow, darker than thallus, plane; margin yellow, concolorous with thallus; epihymenium brownish yellow, 25–50 µm thick; hymenium hyaline, 37.5–62.5 µm high; paraphyses simple, with 4–5 septa, apices often expanded; hypothecium hyaline, 50–87.5 µm high; asci clavate, 37.5–55 × 12.5–20 µm, ±100-spored; ascospores hyaline, ellipsoidal, aseptate, 5–6 × 2–3 µm. Pycnidia immersed; conidia bacilliform, 2–2.5 × 1 µm.

Chemistry. Thallus UV+ dark orange-yellow, P–, K–, C–, KC–. Containing rhizocarpic acid.

Distribution and ecology. This species usually grows on exposed rocks in the Gobi, desert steppe, and in bush formations between ca 1290 m and ca 2190 m. It is distributed in the Qinghai, Xinjiang, and Ningxia provinces in China.

Etymology. The epithet "*corrugatulum*" refers to the wrinkled surface of the species.

Note. It is characterized by the absence of apothecia in most examined specimens, wrinkled surface, rugose lobes, numerous pycnidia, and absence of fatty acids. *Pleopsidium gobiense* also lacks fatty acids but frequently develops apothecia with flat surfaces.

Selected specimens examined. China. • **Ningxia Prov.:** Yinchuan Ci., Gunzhongkou Scenic Spot, 26 Jul. 2021, Y.J. Zhang ZYJ1 (KUN); • Helan Mount Nature Reserve, Suyukou Forest Park, 38°44'13"N, 105°57'10"E, alt. 1640 m, 19 Aug. 2015, Abdulla Abbas 20151024-a (XJU); • Helan Mount Nature Reserve, 38°44'06"N, 105°57'10"E, alt. 1650 m, 13 Aug. 2015, Abdulla Abbas 20151086-c (XJU). • **Xinjiang Prov.:** Hami Ci., Balikun Co., G335, 43°36'09"N, 92°44'45"E, alt. 1639 m, 04 Jul. 2022, L.S. Wang et al. 22-72992 (KUN); • Hami Ci., Balikun Co., Sa'erqiaoke Vil., 43°45'57"N, 92°02'26"E, 04 Jul. 2022, L.S. Wang et al. 22-72341 (KUN); • Fuhai Co., Hongshanzui, alt. 2000 m, 3 Oct. 2000, Abdulla Abbas Po001003 (XJU); • Yili Region, Altay Qinggou, alt. 1294 m, 17 June 2017, Abdulla Abbas 20130708-1 (XJU).

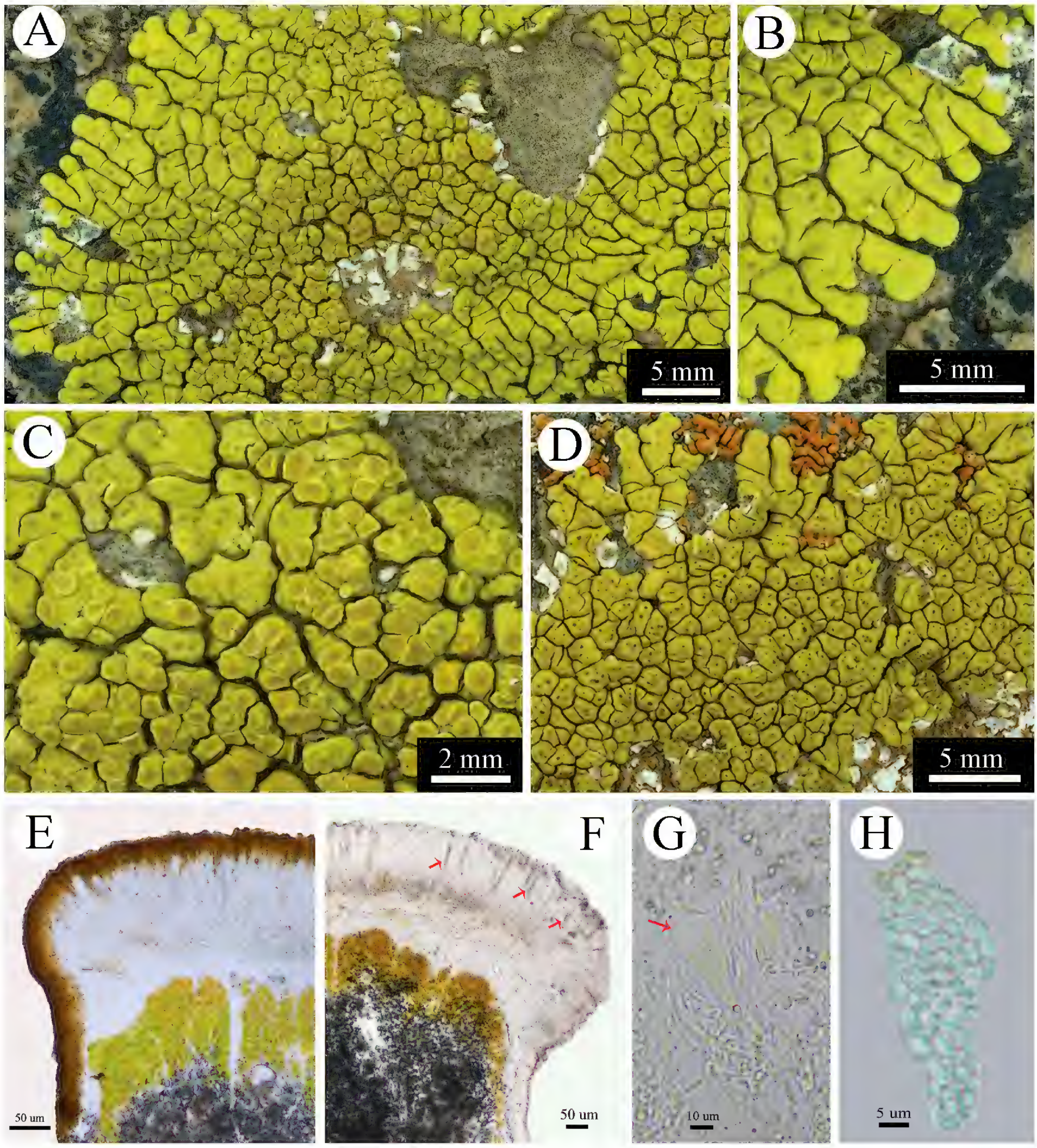

Figure 5. *Pleopsidium corrugatulum* (ZSB23-906 KUN). **A.** Thallus; **B.** Lobes; **C.** Apothecia; **D.** Pycnidia; **E, F.** Section of apothecium; **G.** Ascus containing ascospores; **H.** Simple ascospores. Scale bars: 5 μm (**H**); 10 μm (**G**); 50 μm (**E, F**); 2 mm (**C**); 5 mm (**A, B, D**).

Pleopsidium tumidulum **M. Ai, Xin Y. Wang & Li S. Wang, sp. nov.**

MycoBank No: 859409

Figs 6, 7

Type. China. • Qinghai Prov.: Dulan Co., Xiangjia Vil., 36°12'19"N, 97°01'00"E, alt. ca 2850 m, on rock, 15 Sep. 2020, L.S. Wang et al. 20-67124 (holotype: KUN; isotype: SDNU).

Diagnosis. The new species differs from other *Pleopsidium* species by lacking fatty acids, having thick thalli, convex, plump, and swollen lobes, and by molecular data.

Description. Thallus crustose, tightly attached to the substrate, areolate at center, radiate-plicate at margins; areoles approximately uniform, closely linked, fertile, 1.5–2.5 × 1.0–1.8 mm; marginal lobes long, convex, and plump, 2.5–4.5 mm long, 0.8–2.5 mm wide, 1.5–3.0 mm thick, tightly attached to the substrate; the apices of marginal lobes have lower cortex; upper surface bright yellow with rhizocarpic acid in cortex, smooth, becoming convex when mature; upper cortex yellow, 25–37.5 µm thick; algal layer 62.5–100 µm thick; medulla white, more than 87.5 µm thick; areoles at the center without the lower cortex. Apothecia numerous, one apothecia in each areola, cryptolecanorine to lecanorine, roundish, 1.3–2.5 mm in diam.; disc yellow, darker than thallus, plane to slight convex; margins yellow, concolorous with thallus; epihymenium brownish yellow, 25–37.5 µm thick; hymenium hyaline, 100–112.5 µm high; paraphyses simple, with 4–5 septa, apices often expanded; hypothecium hyaline, 50–62.5 µm high; asci clavate, 37.5–55 × 17.5–25 µm, ±100-spored; ascospores hyaline, ellipsoidal, aseptate, 4–5 × 2–3 µm. Pycnidia immersed; conidia bacilliform, 2–3 × 1 µm.

Chemistry. Thallus UV+ dark orange-yellow, P–, K–, C–, KC–. Containing rhizocarpic acid and an unknown acid (trace).

Distribution and ecology. This species usually grows on exposed rocks in the Gobi, desert steppe, and in bush formations at elevations between ca 1540 m and ca 3470 m. It is distributed in the Qinghai, Xinjiang, and Neimenggu provinces in China.

Etymology. The epithet "*tumidulum*" refers to its plump and swollen lobes.

Note. It is morphologically similar to *Pleopsidium gobiense* and *P. corrugatulum*, but *P. tumidulum* has thicker and smoother thalli (up to 3 mm thick), longer

Figure 6. *Pleopsidium tumidulum* in its habitat (18-59258 KUN).

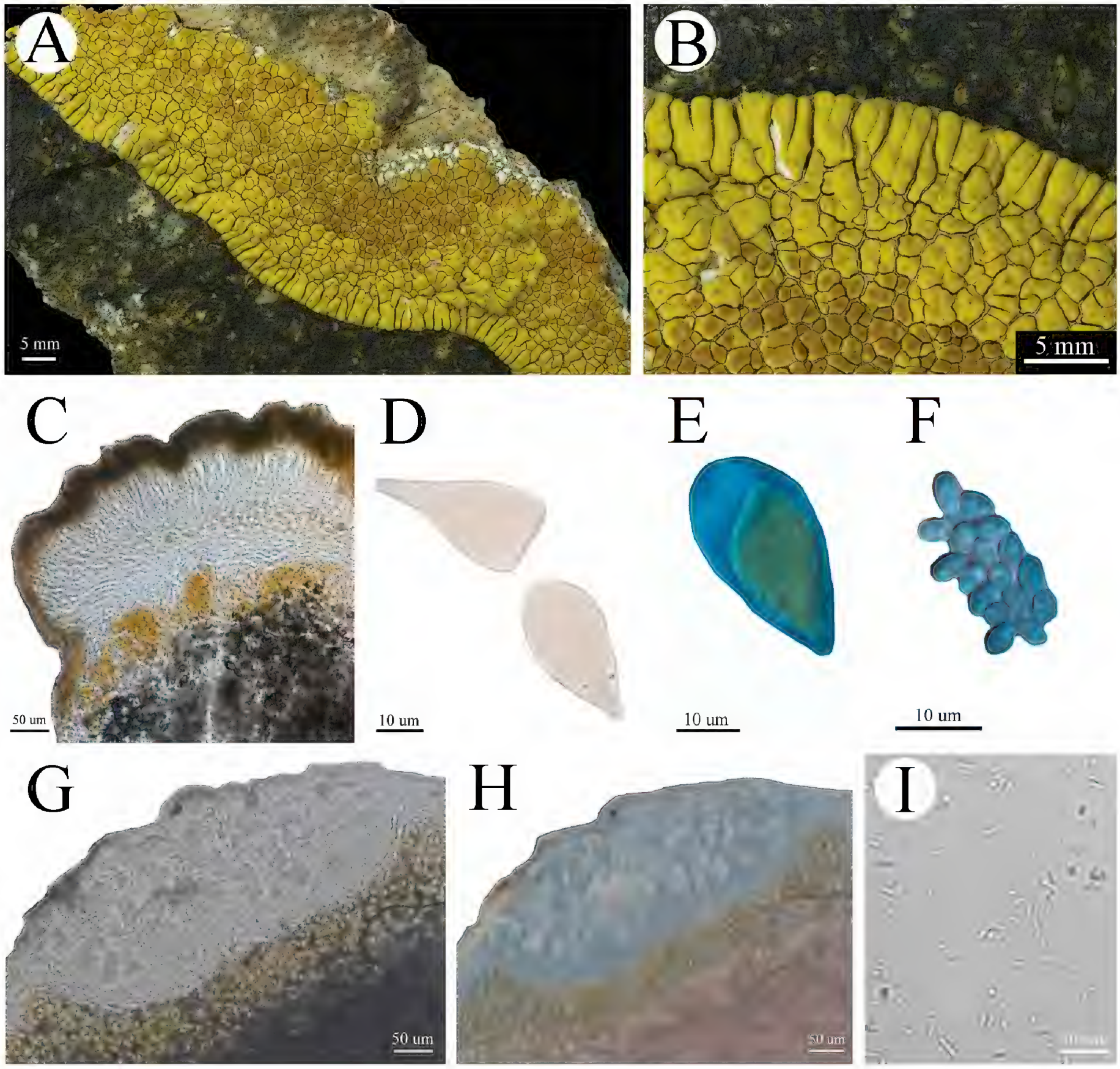

Figure 7. *Pleopsidium tumidulum* (20-67124 KUN). **A.** Thallus; **B.** Lobes and apothecia; **C.** Section of apothecium; **D, E.** Young asci; **F.** Simple ascospores; **G, H.** Section of pycnidia; **I.** Conidia. **E, F, H** were captured under polarized light. Scale bars: 10 μm (**D, E, F, I**); 50 μm (**C, G, H**); 5 mm (**A, B**).

marginal lobes (up to 4.5 mm long), bigger apothecia (over 1.5 mm), and smaller ascospores (less than 5 μm long). The new species differs from clade 2 *Pleopsidium* species (*P. discurrens*, *P. chlorophanum*, and *P. flavum*) in lacking fatty acids.

Selected specimens examined. China. • **Neimenggu Prov.:** Huhehaote Ci., Luotuogou Vil., 42°56'22"N, 86°09'05"E, alt. 2680 m, 11 Aug. 2012, Lazzat Nurtai 20121958-1 (XJU); • Alxa Youqi, 39°04'27"N, 101°01'10"E, alt. 2307 m, 17 Aug. 2015, Lazzat Nurtai 20157527-1 (XJU). • **Qinghai Prov.:** Wulan Co., Gobi desert along the way from Chaka to Wulan, 36°52'18"N, 98°55'45"E, alt. 3191 m,19 May 2018, L.S. Wang et al. 18-58228 (KUN); • Wulan Co., Gobi desert along the way from Chaka to Wulan, 36°52'18"N, 98°55'45"E, alt. 3151 m, 19 May 2018, L.S. Wang et al. 18-59258 (KUN); • Wulan Co., Dulan Lake, 36°48'34"N, 98°27'06"E, alt. 2905 m, 25 Mar. 2023, S.B. Zhang et al. ZSB23-545 (KUN); • Wulan Co., Halihatu Forest Park, 37°00'41"N, 98°40'27"E, alt. 3215 m, 24 Mar. 2023, S.B. Zhang et al. ZSB23-538 (KUN); • Dulan Co., Kaoxiaotu Scenic Spot, 36°07'03"N, 98°06'23"E, alt. 3399 m, 20

Apr. 2024, S.B. Zhang et al. ZSB24-1392 (KUN); • Dulan Co., Reshui Vil., 36°13'02"N, 98°09'07"E, alt. 3245 m, 20 Apr. 2024, S.B. Zhang et al. ZSB24-1400 (KUN); • Dulan Co., Xiangjia Vil., 36°12'19"N, 97°01'00"E, alt. 2856 m, 15 Sep. 2020, L.S. Wang et al. 20-67122 (KUN); • Datong Co. Xiegou Vil., 36°55'42"N, 101°32'12"E, alt. 3090 m, 04 Mar. 2025, S.B. Zhang et al. ZSB25-2149 (KUN); • Dachaidan Administrative District, Snow Mountain Hot Spring Tourist Resort, 37°56'00"N, 95°22'54"E, alt. 2593 m, 16 Sep. 2023, S.B. Zhang et al. ZSB23-1219 (KUN); • Delingha Ci, Cypress Mountain, 37°28'34"N, 97°21'37"E, Alt. 3469 m, 17 Apr. 2024, S.B. Zhang et al. ZSB24-1363 (KUN). • **Xinjiang Prov.:** Hami Ci., Balikun Co., Haiziyan Vil., 43°35'49"N, 92°46'28"E, alt. 1543 m, 05 Sep. 2023, S.B. Zhang et al. XJ-ZSB23-041 (KUN); • Hejing Co., G218, 42°59'40"N, 86°06'22"E, alt. 3003 m, 01 Jul. 2022, L.S. Wang et al. 22-72854 (KUN); • Hejing Co., G218, 42°54'22"N, 86°17'37"E, alt. 2221 m, 01 Jul. 2022, L.S. Wang et al. 22-72874 (KUN); • Hejing Co., G218, 42°54'23"N, 86°17'39"E, alt. 2234 m, 01 Jul. 2022, D. Liu LD22-468 (KUN); • Hejing Co., Tianshan Mountain, 42°50'40"N, 86°21'05"E, alt. 1951 m, 29 Jun. 2022, Y.Y. Zhang ZYY22-558 (KUN), L.S. Wang et al. 22-71718 (KUN); • Hejing Co., Baluntai Town, 42°51'50"N, 86°26'35"E, alt. 2036 m, 02 Jul. 2022, X.Y. Wang et al. XY22-896 (KUN); • Hejing Co., Baluntai Town, 42°50'40"N, 86°21'06"E, alt. 1904 m, 29 Jun. 2022, X.Y. Wang et al. XY22-773 (KUN), L.S. Wang et al. 22-72216 (KUN).

Pleopsidium discurrens (Zahlbr.) Obermayer, Annales Botanici Fennici 33(3): 232 (1996)

Fig. 8

≡ *Acarospora* (sect. *Pleopsidium*) *discurrens* A. Zahlbr. in Handel-Mazzetti, Symbolae Sinicae, Pars III:140-141, 1930.[1]

Ind Loc. "China. Prov. Yünnan [=Yunnan] bor.-occid.: In montis Yülung-schan prope urbem Lidjiang ("Likiang") regione alpina, ad rupes inter pratum Latuka et alveum Schitako. Substr. schisto argilloso, alt. s. m. ca. 4000 m, leg. 20. VII. 1914, Dr. Heinr. Frh. v. Handel-Mazzeni. (Diar. Nr. 676). det. Zahlbruckner Nr. 4297. (lectotype: WU; isolectotype: W)".

Note. *Pleopsidium discurrens* was described from Yulong Snow Mountain of Yunnan and Sichuan and then later also found in Xizang (Zahlbruckner 1930; Obermayer 1996). It was defined as having typical ribbon-like, elongate, branched, and spreading lobes (Fig. 8B). However, in combination with molecular systematics, this species shows extensive intraspecific morphological variation (Fig. 8). The specimens from northwestern Yunnan often have typical lobes (Fig. 8A, B), while lobes of specimens from Xizang are non-branched (Fig. 8E, F).

Selected specimens examined. China. • **Yunnan Prov.:** Deqing Co., Baima Snow Mountain, 28°23'17"N, 99°01'10"E, alt. 4400 m, 01 Nov. 2015, L.S. Wang et al. 15-49590 (KUN); • Deqing Co., Baima Snow Mountain, 28°23'17"N, 99°01'02"E, alt. 4519 m, 4 Jul. 2012, L.S. Wang et al. 12-34822 (KUN); • Lijiang Ci., Yulong Naxi Autonomous Co., Yulong Snow Mountain, 27°01'56"N, 100°11'20"E, alt. 3737 m, 24 Oct. 2017, A.C. Yin 17-56207 (KUN); • Lijiang Ci., Laojunshan Mountain, 26°38'30"N, 99°43'47"E, alt. 3855 m, 28 Sep. 2018, L.S. Wang et al. 18-60699 (KUN); • Shan-

1 For a detailed description, see Obermayer (1996).

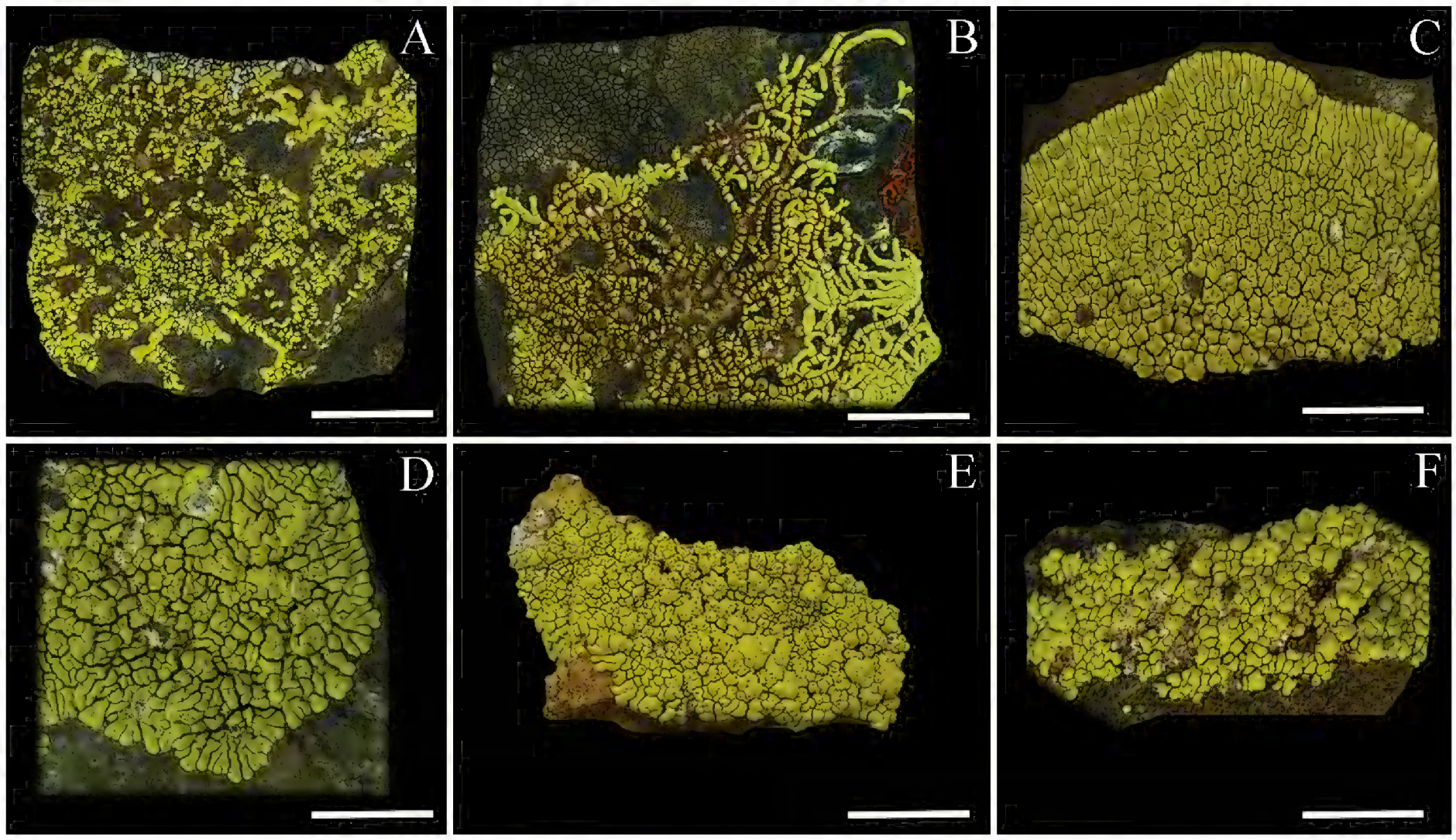

Figure 8. Intraspecific morphological variation of *Pleopsidium discurrens*. **A.** 15-49590 (KUN), Yunnan; **B.** 17-56207 (KUN), Yunnan; **C** 17-55054 (KUN), Yunnan; **D.** 19-65758 (KUN), Xizang; **E.** 19-64991 (KUN), Xizang; **F.** 19-63913 (KUN), Xizang. Scale bars: 5 mm.

gri-la Ci., on the way from Shangri-La to Daocheng, 28°26'00"N, 100°13'38"E, alt. 2951 m, 2 Jun. 2023, L.S. Wang et al. 23-74275 (KUN); • Shangri-la Ci., on the way from Shangri-La to Daocheng, 28°26'00"N, 100°13'39"E, alt. 2981 m, 2 Jun. 2023, L.S. Wang et al. 23-74395 (KUN); • Kunming Ci., Dongchuan District, Guniuzhai Mountain Scenic Spot, 26°10'01"N, 103°13'33"E, alt. 3190 m, 10 May. 2017, L.S. Wang et al. 17-55117 (KUN); • Kunming Ci., Dongchuan District, Guniuzhai Mountain Scenic Spot, 26°09'50"N, 103°13'31"E, alt. 3100 m, 10 May. 2017, L.S. Wang et al. 17-55054 (KUN). • **Xizang Prov.:** Zuogong Co., on the way from Rumei to Zuogong, at the 3550 milestone on G318, 29°43'16"N, 98°01'34"E, alt. 4968 m, 21 Sep. 2016, L.S. Wang et al. 16-53097 (KUN); • Dingri Co., Zhaguo Vil., 28°35'25"N, 86°53'58"E, alt. 4298 m, 27 Jul. 2019, L.S. Wang et al. 19-65574 (KUN); • Nielamu Co., Yalai Vil., 28°21'52"N, 86°05'44"E, alt. 4402 m, 26 Jul. 2019, L.S. Wang et al. 19-64991 (KUN); • Nielamu Co., 28°21'51"N, 86°05'42"E, alt. 4382 m, 26 Jul. 2019, L.S. Wang et al. 19-64053 (KUN); • Cuoqin Co., S206, 31°03'34"N, 85°02'11"E, alt. 4839 m, 20 Jul. 2019, L.S. Wang et al. 19-63666 (KUN); • Pulan Co., La'angcuo Lake, 30°34'50"N, 81°15'25"E, alt. 4628 m, 24 Jul. 2019, L.S. Wang et al. 19-63913 (KUN), L.S. Wang et al. 19-63921 (KUN); • Dingjie Co., Chentang Town, 27°55'48"N, 87°37'57"E, alt. 4243 m, 28 Jul. 2019, L.S. Wang et al. 19-65758 (KUN).

***Pleopsidium gobiense* (H. Magn.) Hafellner, Nova Hedwigia 56(3–4): 294 (1993)**

MycoBank No: MBT 10027662

Fig. 9

≡ *Acarospora gobiensis* H. Magn., K. Svenska Vetensk-Akad. Handl., Ser. III 7(4): 98, 1929.

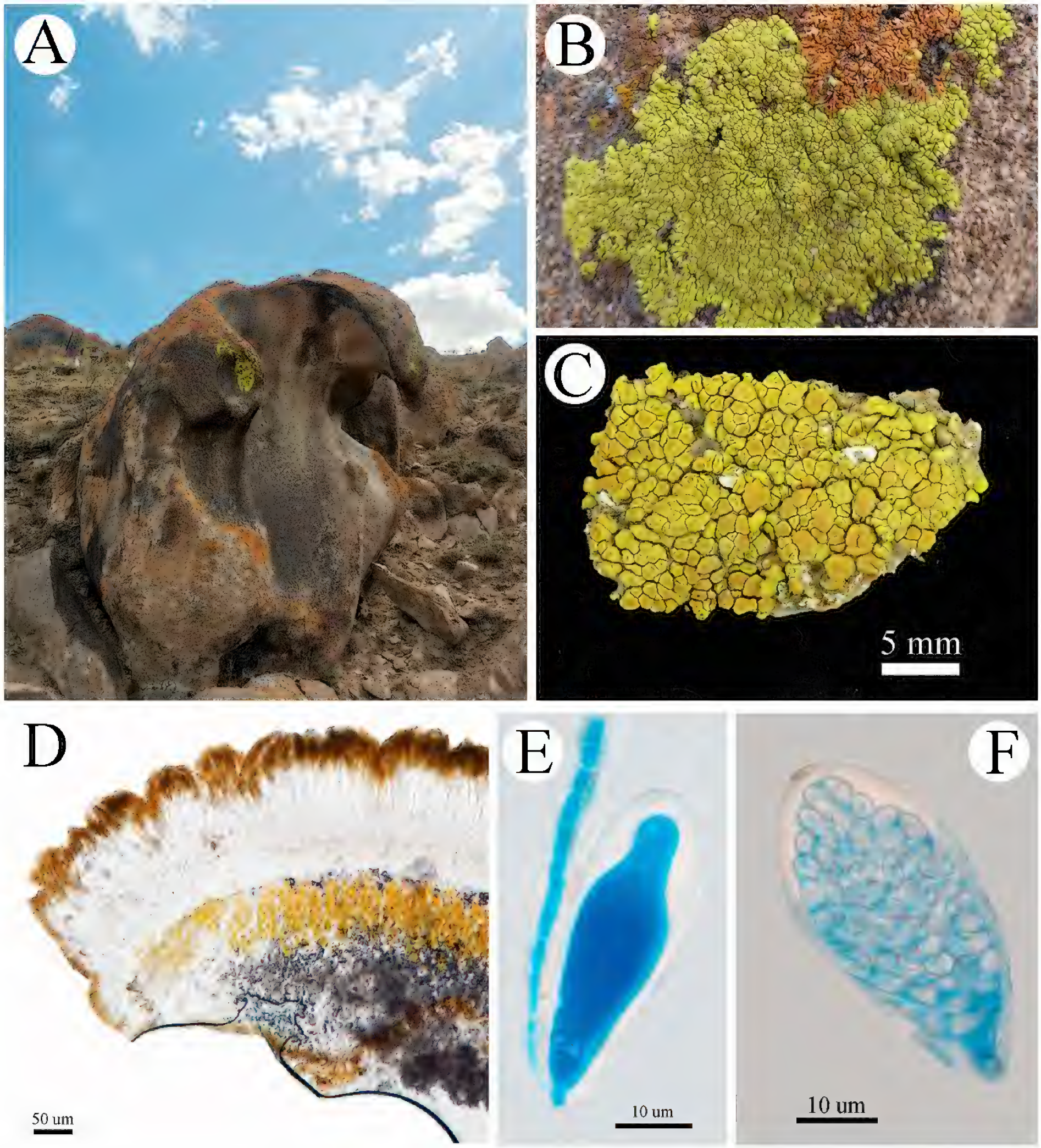

Figure 9. *Pleopsidium gobiense* (neotype, XY22-947 KUN). **A.** General habitat; **B.** Thallus; **C.** Apothecia; **D.** Section of apothecium; **E.** Young ascus and paraphysis; **F.** Simple ascospores. **E, F** were stained with Lugol's iodine solution. Scale bars: 10 μm (**E, F**); 50 μm (**D**); 5 mm (**C**).

Ind Loc. "Gobi Wüste, Lage VII SO von Chami 1895 Futterer".

Type. • China. Xinjiang Prov.: Hami Ci., Balikun Co., Haiziyan Vil., 43°36'10"N, 92°44'43"E, alt. ca 1570 m, on rock, 04 Jul. 2022, X.Y. Wang et al. XY22-947 (neotype: KUN, designated here; isoneotype: SDNU).

A more detailed description is in Magnusson (1929).

Note. The type specimen was originally deposited at the Botanical Museum in Berlin-Dahlem (Magnusson 1929) but has unfortunately been lost during World War II (Dr. Bibiana Moncada, curator of the Herbarium of the Botanischer

Garten Berlin (B), personal communication). According to the protologue, the original specimen was collected from Hami (historically referred to as "Chami") in China. Based on the original description, ecology, chemistry, and specimens from Hami, we confirmed the taxonomic identity of this species and provided supporting molecular data. In addition to its occurrence in Xinjiang, this species is also distributed in Gansu, Qinghai, and Neimenggu provinces in China (Magnusson 1940, 1944).

Selected specimens examined. China. • **Xinjiang Prov.:** Hami Ci., Balikun Co., G335, 43°36'10"N, 92°44'44"E, alt. 1634 m, 4 Jul. 2022, L.S. Wang et al. 22-72982 (KUN); • Hami Ci., Balikun Co., Haiziyan vil., 43°36'08"N, 92°44'42"E, alt. 1663 m, 4 Jul. 2022, D. Liu LD22-513 (KUN); • Zhaosu Co., Yuhu Lake, 81°03'03"N, 42°44'03"E, alt. 2010 m, 14 Sep. 2023, S.B. Zhang et al. XJ-ZSB23-119 (KUN).

Key to the species of *Pleopsidium*

1 Thallus with fatty acid(s) **2**
– Thallus without fatty acid(s) **4**
2 Areoles elongated with distinctly radiating branches or not, thallus thin, distributed in alpine areas of Asia ..... ***P. discurrens***
– Without distinctly radiating elongated areoles, distributed in Europe and North America **3**
3 Apothecia 1–3 mm in diam ..... ***P. chlorophanum***
– Apothecia less than 1 mm in diam ..... ***P. flavum***
4 Thallus up to 3.0 mm thick, areoles convex and plump, lobes smooth and up to 4.5 mm long ..... ***P. tumidulum***
– Thallus less than 1.5 mm thick, areoles wrinkled, lobes less than 3 mm long **5**
5 Apothecia frequent and plane, nearly flat to the thallus, pycnidia rare ..... ***P. gobiense***
– Apothecia rare, pycnidia frequent ..... ***P. corrugatulum***

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Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

Use of AI

No use of AI was reported.

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Author contributions

Min Ai: Writing-manuscript draft, data curation, experiment, species identification. Cong Cong Miao: Writing-original draft, data curation, experiment. Fiona Ruth Worthy: Manuscript revision and language polishing. Lazzat Nurtai, De Ning Zhang, Sheng Bang Zhang, Gui Lan Han: Providing specimens. Li Song Wang: Data Investigation Xin Yu Wang: Writing-review and editing.

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Data availability

All of the data that support the findings of this study are available in the main text or Supplementary Information.

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Supplementary material 1

The sequence of phylogenetic analysis: nuITS dataset

Authors: Min Ai, Cong Cong Miao, Fiona Ruth Worthy, Lazzat Nurtai, De Ning Zhang, Sheng Bang Zhang, Gui Lan Han, Li Song Wang, Xin Yu Wang

Data type: txt

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Link: https://doi.org/10.3897/mycokeys.120.161566.suppl1

Supplementary material 2

The sequence of phylogenetic analysis: nuLSU dataset

Authors: Min Ai, Cong Cong Miao, Fiona Ruth Worthy, Lazzat Nurtai, De Ning Zhang, Sheng Bang Zhang, Gui Lan Han, Li Song Wang, Xin Yu Wang

Data type: txt

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Supplementary material 3

The sequence of phylogenetic analysis: the 3-locus concatenated matrix (nuITS-mtSSU-nuLSU)

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Supplementary material 4

BLASTn results for the nuLSU barcode sequences

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Data type: docx

Explanation note: BLASTn results for the nuLSU barcode sequences designed for three species without fatty acids within *Pleopsidium*, under a scenario of corrected reference sequence labels (right annotation) based on phylogenetic inferences. Top-scoring hits are ranked by E-value and results with the lowest value are highlighted.

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